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SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd AND Pig Research and Development Corporation

<120> Novel lawsonia spp. gene and uses therefor II

<130> p:\oper\mro\lawson-2.pct

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<150> US 60/133,982

<151> 1999-05-12

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 186

<212> PRT

<213> Lawsonia intracellularis

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Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
35 40 45

Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
50 55 60

Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
65 70 75 80

Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
85 90 95

Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
100 105 110

Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
115 120 125

Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
130 135 140

Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr

10018290.041602

- 2 -

Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
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Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
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gct aac agt gca ttt tcg gct gac ttc cct att ggt gtc ttt aat tct 96
 Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
 20 25 30

caa tcc att gcc atg gag agt gaa gca gct aag gcc gct caa aaa aaa 144
 Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
 35 40 45

tta caa tca gaa ttt ggt aat gaa aaa aca caa ctt gaa aaa caa gca 192
 Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
 50 55 60

aaa gat ttg caa aca aaa gct gat gat tta caa gct aag tca gca gct 240
 Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
 65 70 75 80

atg tct aac caa gca cgt gaa gat aaa caa aga gaa ttt ctt gaa ctt 288
 Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
 85 90 95

cgt cgt aat ttc gaa gaa aaa tct cgt gac ttt gca ata cgt gtc gaa 336
 Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
 100 105 110

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- 3 -

caa gct gaa aac aca tta cgt caa tat cta gct gaa caa acc tat ctt 384
 Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
 115 120 125

gct gct gaa act ata gca aaa aag aaa ggg tta aaa ctt gtt ctt gat 432
 Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
 130 135 140

agt gct agt gga agt gta atg tac ctt gaa aaa aat cta gat att aca 480
 Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
 145 150 155 160

aaa gaa att ctt gaa gcc ata aat gct gca tgg aaa aaa ggt gga agt 528
 Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
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 Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
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